

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-15 (Cancelled)

Claim 16 (Previously Presented) A peptide consisting of the formula;



wherein X_1 , X_3 , X_4 and X_5 are each a natural or unnatural amino acid and X_2 is serine or alanine.

Claim 17 (Previously Presented) A peptide according to claim 16, wherein X_5 is selected from isoleucine and glycine.

Claim 18 (Previously Presented) A peptide according to claim 16, wherein X_1 and X_4 are both basic amino acid residues and X_3 is a basic or polar residue.

Claim 19 (Previously Presented) A peptide according to claim 18, wherein X_1 is histidine and X_4 is arginine, and X_3 is lysine or cysteine.

Claim 20 (Currently Amended) A peptide consisting of the formula;



wherein X_1 , X_3 , X_4 and X_5 are each a natural or unnatural amino acid and X_2 is serine or alanine, wherein the peptide is

- (a) modified by deletion of one or more amino acid residues;
- (b) modified by substitution of one or more natural amino acid residues by the corresponding D-stereomer;
- ~~(c)~~ (c) a cyclic;
- ~~(h)~~ (d) modified by reversing the order of the final two residues at the C-terminal end;
- ~~(i)~~ (e) any combination of (a)-~~(h)~~(d).

Claim 21 (Previously Presented) A peptide consisting of the formula;



wherein:

- (a) X_1 is deleted or is a natural or unnatural amino acid,
- (b) X_2 is serine or alanine or a straight or branched chain amino acid,
- (c) X_3 is a basic amino acid or straight chain aliphatic amino acid,
- (d) R is unchanged or conservatively substituted by a basic amino acid,
- (e) X_4 is an amino acid that is capable of providing at least one site for participating in hydrogen bonding,
- (f) L is unchanged or conservatively substituted,
- (g) X_5 is a natural or unnatural amino acid, or
- (h) F is unchanged or substituted by an aromatic amino acid.

Claim 22 (Previously Presented) A peptide consisting of the formula;



wherein

- (a) X_1 is deleted or is a natural or unnatural amino acid residue,
- (b) X_2 is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (c) X_3 is a basic residue, or an uncharged natural or unnatural amino acid residue,
- (d) arginine is replaced by a basic residue or an uncharged natural or unnatural amino acid residue,
- (e) X_4 is a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage,
- (f) leucine is replaced with a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (g) X_5 is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (h) phenylalanine is replaced with a natural or unnatural amino acid,
- (i) X_5 and the terminal phenylalanine residue are reversed, or
- (j) the peptide is in cyclic form by the formation of a linkage between the side chain of X_4 and the C-terminus residue.

Claim 23 (Previously Presented) A peptide according to claim 16, wherein X_2 is alanine.

Claim 24 (Previously Presented) A peptide according to claim 16, wherein X_5 is isoleucine.

Claim 25 (Previously Presented) A peptide selected from the group consisting of:

H S K R R L I F									(SEQ ID No. 34)
H A K R R L I F									(SEQ ID No. 35)
H S K R R L F G									(SEQ ID No. 36)
H A K R R L F G									(SEQ ID No. 37)
K A C R R L F G									(SEQ ID No. 38)
K A C R R L I F									(SEQ ID No. 39)
	X1	X2	X3	R	X4	L	X5	F	
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 28)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 40)
	H-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 41)
H-	Pya-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 42)
H-	Thi-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 43)
H-	Hse-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 44)
H-	Phe-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 45)
H-	Dab-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 46)
H-	His-	Gly-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 47)
H-	His-	Abu-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 48)
H-	His-	Nva-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 49)
H-	His-	Bug-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 50)
H-	His-	Val-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 51)
H-	His-	Ile-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 52)
H-	His-	Phg-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 53)
H-	His-	Phe-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 54)
H-	His-	Ala-	Ala-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 56)
H-	His-	Ala-	Nle-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 57)
H-	His-	Ala-	Abu-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 58)
H-	His-	Ala-	Leu-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 59)
H-	His-	Ala-	Arg-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 60)
H-	His-	Ala-	Lys-	Ala-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 61)
H-	His-	Ala-	Lys-	Cit-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 62)
H-	His-	Ala-	Lys-	Hse-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 63)
H-	His-	Ala-	Lys-	His-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 64)
H-	His-	Ala-	Lys-	Nle-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 65)
H-	His-	Ala-	Lys-	Gln-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 66)
H-	His-	Ala-	Lys-	Lys-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 67)
H-	His-	Ala-	Lys-	Arg-	Ala-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 68)
H-	His-	Ala-	Lys-	Arg-	Asn-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 69)
H-	His-	Ala-	Lys-	Arg-	Pro-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 70)
H-	His-	Ala-	Lys-	Arg-	Ser-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 71)

H-	His-	Ala-	Lys-	Arg-	Aib-	Leu-	Ile-	Phe	-NH2	(SEQ ID No. 72)
H-	His-	Ala-	Lys-	Arg-	Sar-	Leu-	Ile-	Phe	-NH2	(SEQ ID No. 73)
H-	His-	Ala-	Lys-	Arg-	Cit-	Leu-	Ile-	Phe	-NH2	(SEQ ID No. 74)
H-	His-	Ala-	Lys-	Arg-	Arg-	Ala-	Ile-	Phe	-NH2	(SEQ ID No. 76)
H-	His-	Ala-	Lys-	Arg-	Arg-	Ileu-	Ile-	Phe	-NH2	(SEQ ID No. 77)
H-	His-	Ala-	Lys-	Arg-	Arg-	Ile-	Ile-	Phe	-NH2	(SEQ ID No. 78)
H-	His-	Ala-	Lys-	Arg-	Arg-	Val-	Ile-	Phe	-NH2	(SEQ ID No. 79)
H-	His-	Ala-	Lys-	Arg-	Arg-	Nle-	Ile-	Phe	-NH2	(SEQ ID No. 80)
H-	His-	Ala-	Lys-	Arg-	Arg-	Nva-	Ile-	Phe	-NH2	(SEQ ID No. 81)
H-	His-	Ala-	Lys-	Arg-	Arg-	Cha-	Ile-	Phe	-NH2	(SEQ ID No. 82)
H-	His-	Ala-	Lys-	Arg-	Arg-	Phe-	Ile-	Phe	-NH2	(SEQ ID No. 83)
H-	His-	Ala-	Lys-	Arg-	Arg-	1Nap-	Ile-	Phe	-NH2	(SEQ ID No. 84)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ala-	Phe	-NH2	(SEQ ID No. 85)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Leu-	Phe	-NH2	(SEQ ID No. 86)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Val-	Phe	-NH2	(SEQ ID No. 87)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Nle-	Phe	-NH2	(SEQ ID No. 88)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Nva-	Phe	-NH2	(SEQ ID No. 89)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Cha-	Phe	-NH2	(SEQ ID No. 90)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Phe-	Phe	-NH2	(SEQ ID No. 91)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	1Nap-	Phe	-NH2	(SEQ ID No. 92)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Leu	-NH2	(SEQ ID No. 95)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Cha	-NH2	(SEQ ID No. 96)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Hof	-NH2	(SEQ ID No. 97)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Tyr	-NH2	(SEQ ID No. 98)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2	(SEQ ID No. 99)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	mFPhe	-NH2	(SEQ ID No. 100)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Trp	-NH2	(SEQ ID No. 101)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	1Nap	-NH2	(SEQ ID No. 102)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	2Nap	-NH2	(SEQ ID No. 103)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Lys	-NH2	(SEQ ID No. 104)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Tic	-NH2	(SEQ ID No. 105)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	L-Pse	OH	(SEQ ID No. 106)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	D-Pse	OH	(SEQ ID No. 107)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	L-Pse	OH	(SEQ ID No. 108)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	D-Pse	OH	(SEQ ID No. 109)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	L-Psa	OH	(SEQ ID No. 110)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	D-Psa	OH	(SEQ ID No. 111)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	L-Psa	OH	(SEQ ID No. 112)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	D-Psa	OH	(SEQ ID No. 113)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	Dhp	OH	(SEQ ID No. 114)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	Dhp	OH	(SEQ ID No. 115)

H-	His	Ala	Lys	Arg	Arg	Leu	Ile	Pheol	(SEQ ID No. 116)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	Pheol	(SEQ ID No. 117)
H-	Ala-	Ala-	Abu-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 118)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 119)
H-	Ala-	Ala-	Lys-	Arg-	Cit-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 120)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ala-	pFPhe	-NH2 (SEQ ID No. 121)
H-	Ala-	Ala-	Abu-	Arg-	Ser-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 122)
H-	Ala-	Ala-	Lys-	Gln-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 123)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 124)
H-	Gly-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 125)
H-	Ala-	Ala-	Lys-	hArg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 126)
H-	Ala-	Ala-	Lys-	Ser-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 127)
H-	Ala-	Ala-	Lys-	Hse-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 128)
H-	Ala-	Ala-	Lys-	Arg-	Lys-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 129)
H-	Ala-	Ala-	Lys-	Arg-	Orn-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 130)
H-	Ala-	Ala-	Lys-	Arg-	Gln-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 131)
H-	Ala-	Ala-	Lys-	Arg-	Hse-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 132)
H-	Ala-	Ala-	Lys-	Arg-	Thr-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 133)
H-	Ala-	Ala-	Lys-	Arg-	Nva-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 134)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Phg-	Ile-	pFPhe	-NH2 (SEQ ID No. 135)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Met-	Ile-	pFPhe	-NH2 (SEQ ID No. 136)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Ala-	Ile-	pFPhe	-NH2 (SEQ ID No. 137)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Hof-	Ile-	pFPhe	-NH2 (SEQ ID No. 138)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	hLeu-	Ile-	pFPhe	-NH2 (SEQ ID No. 139)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	alle-	Ile-	pFPhe	-NH2 (SEQ ID No. 140)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Gly-	pFPhe	-NH2 (SEQ ID No. 141)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	βAla	pFPhe	-NH2 (SEQ ID No. 142)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Phg-	pFPhe	-NH2 (SEQ ID No. 143)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Aib-	pFPhe	-NH2 (SEQ ID No. 144)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Sar-	pFPhe	-NH2 (SEQ ID No. 145)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Pro-	pFPhe	-NH2 (SEQ ID No. 146)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Bug-	pFPhe	-NH2 (SEQ ID No. 147)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ser-	pFPhe	-NH2 (SEQ ID No. 148)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Asp-	pFPhe	-NH2 (SEQ ID No. 149)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Asn-	pFPhe	-NH2 (SEQ ID No. 150)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pFPhe-	Phe	-NH2 (SEQ ID No. 151)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	diClPhe	Phe	-NH2 (SEQ ID No. 152)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pClPhe-	Phe	-NH2 (SEQ ID No. 153)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	mClPhe	Phe	-NH2 (SEQ ID No. 154)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	oClPhe-	Phe	-NH2 (SEQ ID No. 155)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pIPhe-	Phe	-NH2 (SEQ ID No. 156)

H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	TyrMe-	Phe	-NH2	(SEQ ID No. 157)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Thi-	Phe	-NH2	(SEQ ID No. 158)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Pya-	Phe	-NH2	(SEQ ID No. 159)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	diClPhe	-NH2	(SEQ ID No. 160)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pClPhe	-NH2	(SEQ ID No. 161)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	mClPhe	-NH2	(SEQ ID No. 162)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	oClPhe	-NH2	(SEQ ID No. 163)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phg	-NH2	(SEQ ID No. 164)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	TyrMe	-NH2	(SEQ ID No. 165)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Thi	-NH2	(SEQ ID No. 166)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Pya	-NH2	(SEQ ID No. 167)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Inc	-NH2	(SEQ ID No. 168)

and the cyclic peptides:

5,8-cyclo-[H-His-Ala-Lys-Arg-Lys-Leu-Phe-Gly]

(SEQ ID No. 169)

5,8-cyclo-[H-His-Ala-Lys-Arg-Orn-Leu-Phe-Gly]

(SEQ ID No. 170)

Claims 26-35 (Cancelled)

Claim 36 (Withdrawn – Currently Amended) An assay for the identification of compounds that interact with a cyclin or a cyclin when complexed with the physiologically relevant CDK, comprising;

(a) incubating a candidate compound and a peptide of formula I;

$X_1X_2X_3RX_4LX_5F$ (formula II) (SEQ ID No. 2)

wherein X_1 , X_3 , X_4 and X_5 ~~may be any~~ are each a natural or unnatural amino acid and X_2 is serine or alanine; ~~and variants thereof or a peptide of the formula III or IV:~~

~~— $H'X'_2K'R_4R_2L'X'_5F'$ (formula III) (SEQ ID No. 3) or $H'X'_2K'R_4R_2L'F'X'_5$ (formula IV) (SEQ ID No. 189) or a variant thereof, wherein~~

~~H' is His, nothing, D-His, Ala, Thi, Hse, Phe, or Dab;~~

~~X'_2 is Ala, Ser, Abu, Val;~~

~~K' is Lys, Arg, or Abu;~~

~~R_4 is Arg, Lys, or Gln; and~~

~~R_2 is Arg, forms a cyclic peptide with the C-terminal residue, Ser, or Cit;~~

~~L' is Leu or Ile;~~

~~X'_5 is Ile, Leu, Gly, or Ala;~~

~~F' is Phe, para-fluoroPhe, meta-fluoroPhe, L-Psa, 2-Nap, Dhp, or D-Psa.~~

and a cyclin or cyclin/CDK complex;

(b) detecting binding of either the candidate compound or the peptide of formula II ~~or III~~ with cyclin.

Claims 37 -40 (Cancelled)

Claim 41 (Withdrawn – Currently Amended) An assay according to claim ~~35~~ 36, wherein the cyclin is selected from cyclin A, cyclin E or cyclin D.

Claim 42 (Withdrawn - Currently Amended) An assay according to claim 41 wherein the cyclin is cyclin A.

Claim 43 (Cancelled)

Claim 44 (Withdrawn - Currently Amended) An assay according to claim ~~35~~ 36, wherein at least one of the assay components is bound to a solid phase.

Claim 45 (Withdrawn) An assay according to claim 44, wherein the p21 derived peptide is labeled such as to emit a signal when bound to said cyclin.

Claim 46 (Withdrawn) An assay according to claim 44, wherein the cyclin is labeled such as to emit a signal when bound to the p21 derived peptide.

Claim 47 (Withdrawn) An assay according to claim 45, wherein one of the assay components is labeled with a fluorescence emitter and the signal is detected using fluorescence polarisation techniques.

Claim 48 (Withdrawn - Currently Amended) A method of using a cyclin in a drug screening assay comprising:

(a) selecting a candidate compound by performing rational drug design with a three-dimensional model of said cyclin, wherein said selecting is performed in conjunction with computer modeling;

- (b) contacting the candidate compound with the cyclin; and
- (c) detecting the binding affinity of the candidate compound for the cyclin groove; wherein a potential drug is selected on the basis of its having a greater affinity for the cyclin groove than that of a peptide of formula II;

$X_1X_2X_3RX_4LX_5F$ (formula II) (SEQ ID No. 2)

wherein X_1 , X_3 , X_4 and X_5 may be any are each a natural or unnatural amino acid and X_2 is serine or alanine; and variants thereof or a peptide of formula III or IV;

~~$H'X'_2K'R_1R_2L'X'_sF'$ (formula III) (SEQ ID No. 3) or~~

~~$H'X'_2K'R_1R_2L'F'X'_s$ (formula IV) (SEQ ID No. 189) or a variant thereof,~~

wherein

~~H' is His, nothing, D-His, Ala, Thi, Hse, Phe, or Dab;~~

~~X'_2 is Ala, Ser, Abu, Val;~~

~~K' is Lys, Arg, or Abu;~~

~~R_1 is Arg, Lys, or Gln; and~~

~~R_2 is Arg, forms a cyclic peptide with the C-terminal residue, Ser, or Cit;~~

~~L' is Leu or Ile;~~

~~X'_s is Ile, Leu, Gly, or Ala;~~

~~F' is Phe, para-fluoroPhe, meta-fluoroPhe, L-Psa, 2-Nap, Dhp, or D-Psa.~~

Claim 49-54 (Cancelled)

Claim 55 (Previously Presented) A peptide according to claim 22, wherein X_1 is selected from the group consisting of histidine, alanine, 3-pyraldylalanine (Pya), 2-thienylalanine (Thi), homoserine (Hse), phenylalanine and diaminobutyric acid (Dab).

Claim 56 (Previously Presented) A peptide according to claim 22, wherein X_2 is selected from the group consisting of alanine, glycine, aminobutyric acid (Abu), norvaline (Nva), t-butylglycine (Bug), valine, phenylglycine (Phg) and phenylalanine.

Claim 57 (Previously Presented) A peptide according to claim 22, wherein X₃ is selected from the group consisting of lysine, arginine, norleucine (Nle), aminobutyric acid (Abu) and leucine.

Claim 58 (Previously Presented) A peptide according to claim 22, wherein arginine is replaced by lysine, citrulline (Cit), homoserine, histidine, norleucine (Nle) or glutamine.

Claim 59 (Previously Presented) A peptide according to claim 22, wherein X₄ is selected from the group consisting of arginine, asparagines, praline, serine, aminoisobutyric acid (Aib), sarcosine, lysine and ornithine.

Claim 60 (Previously Presented) A peptide according to claim 22, wherein leucine is replaced by norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine or 1-naphthylalanine (1Nal).

Claim 61 (Previously Presented) A peptide according to claim 22, wherein X₅ is selected from the group consisting of isoleucine, norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).

Claim 62 (Previously Presented) A peptide according to claim 22, wherein phenylalanine is replaced by leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, para-fluorophenylalanine (pFPhe), meta-fluorophenylalanine (mFPhe), tryptophan, i-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), biphenylalanine (Bip) or (Tic).